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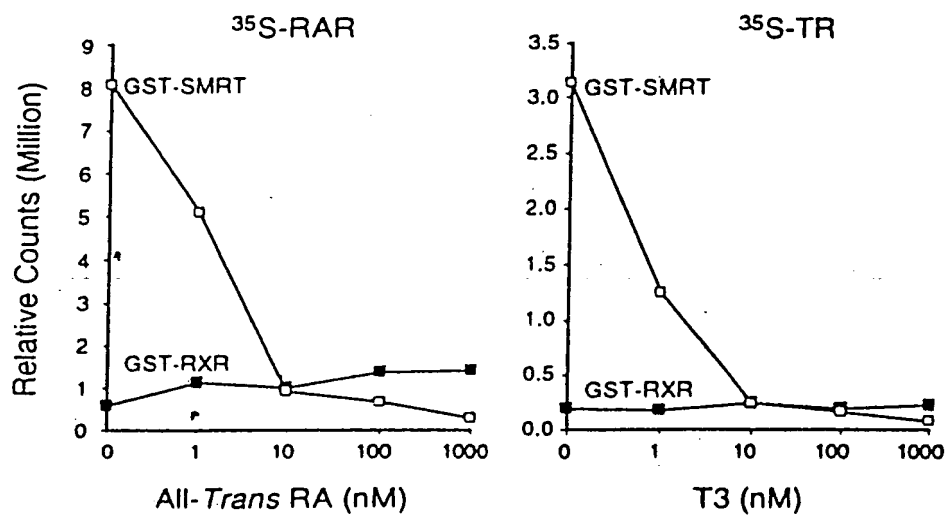


FIGURE 1



1 MEAWDAH@KEAFAAEAQKLEGGDEBCWTSGL@FEV@PREVIKAS@HAP@  
51 SAFSYA@B@GH@L@LGLHDTAR@V@L@P@T@ISN@L@LISSAKH@SVLERQI  
101 GAISQGMSVQLHV@YSEHAKA@V@G@V@TMGL@L@M@D@KKLA@FSGVKQEQ  
151 SPRGQAGPPESLGVPTAQEASVLRGTALGSPVPGGSITKGIPSTRVPSDSA  
201 ITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEG  
251 KKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAI  
301 SSASIEGLMGRAIPPERHSPHHLKEQHHRGSITQGIPRSYVEAQEDYLR  
351 REAKLLKREGTPPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAG  
401 RSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHD  
451 VRSLIGSPGRTFFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSI  
501 ARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEG  
551 SLSSSKASQDRKLTSTPREIAKSPHSTVPEHHHPHISPYEHLRGVSGVD  
601 LYRSHIPLAFDPTSI PRGIPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRG  
651 YPDAALENRQTIINDYITSQQMHNTATAMAQRADMLRGLSPRESSLAL  
701 NYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRH  
751 SSSPLSPGGPHTLTKPTTTSSSERERDRDRERDREREKSILTSTTTVE  
801 HAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPISPRQDALQ  
851 QRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLG  
901 GTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFKAPPARSGLEPA  
951 SSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASDPH  
1001 REKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPK  
1051 HLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPES@PSSSPLI@  
1101 APGVKGH@RVVTLA@HISEVIT@DYTRHHE@LSAPLPAPLYSFPGASCP  
1151 VLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGI  
1201 EPVSPPEGMTPEGHSRSVAVYLLYRDGEQTEPSRMGSKSPGNTSQPPAFF  
  
1251 SK@TESNSA@KSKKQ@INKKLNT@NRNEPEYNISQPGTEIFNMPAITGT  
  
1301 GL@TYRSQA@EHASTNMGLEAIIRKALM@KYDQW.EESPPLSANAFNPL  
  
1350 NASASLPAAMPITAADGRSDHTLTSP).GGGGKAKVSGRPSSRKAKSPAPG  
  
1399 LA..SGDRPPSVSSVHSEGDENRRTPLTNRVWEDRPSSAGSTPFPYNPL@  
  
1447 MRLQAG@MASPPPPG@PAGSG@..AGPHHA...WDEEPKPL@CSQYET@

FIGURE 2



FIGURE 3A

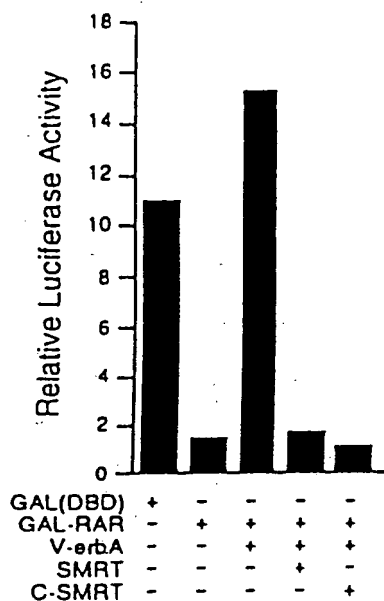


FIGURE 3B

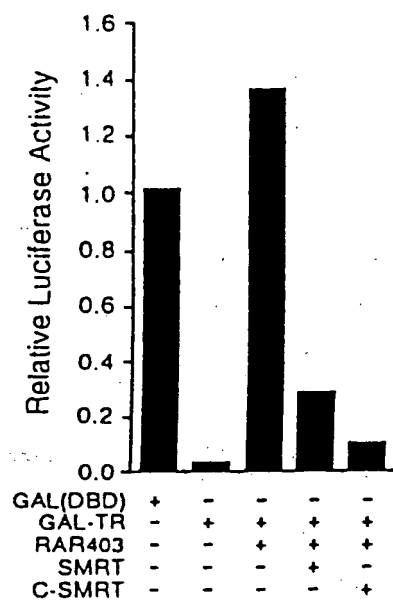


FIGURE 3C

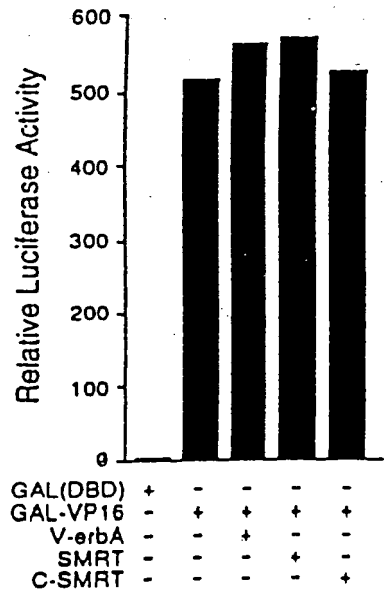
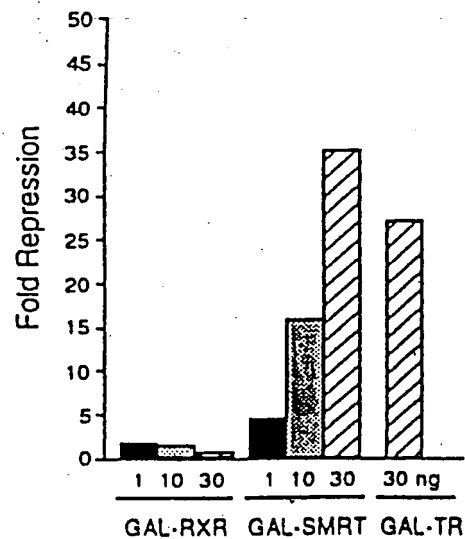


FIGURE 3D





MSGSTQLVAQTWRATEPRYPHSLSYVQIARTHTDVGLLLEYQHHSRDYASHLSPGSI IQPQRRRPSLLSEFPQGNERSQELHLRPESHYSYLPGLKSEM  
MSGSTQPVAQTWRAAEPRYPHSGISYVQIARSHTDVGLLLEYQHHPDYTHSLSPGSI IQPQRRRPSLLSEFPQGSERSQELHLRPESRTFLPELGPDI

101 EFIESKRPRLELLPDPLLRPSLLATGQPSGSEDLTKDRSLTGKLEPVSPSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKKKKQQQL  
101 EFTESKRPRLELLPDPLLRPSLLATGQPSGSEDLTKDRSLAGKLEPVSPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKKKKQQQL

201 EEEAAKPEPEKPVSPPIESKHSRLVQIIYDENRKAEEAHRILEGLGPQVELFLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKPCQ  
201 EEEAAKPEPEKPVSPPIESKHSRLVQIIYDENRKAEEAHRILEGLGPQVELFLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWEQRFQ

301 RYDQLEALEKKVERIENNPRRAKESKVREYEEKQFPEIRKQRELQERMQSRVQGRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMY  
301 RYDQLEAWEKKVERIENNPRRAKESKVREYEEKQFPEIRKQRELQERMQSRVQGRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMY

401 DADQQRIFKFINMGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKNGFLIASFLERKTVAECVLYYYLTKKNYKSLVRRSYRRRGKSQQQQQQQ  
401 DADQQRIFKFINMGLMDDPMKVYKDRQVTNMWSEQERDTFREKFMQHPKNGFLIASFLERKTVAECVLYYYLTKKNYKSLVRRSYRRRGKSQQQQQQQ

501 QQQQQQQQQPMPRSSQEEKDEKEKEKEAEKEEKEPEVENDKEDLLKEKTDGSDNDEKEAVASKGRKTANSQGRRKGRITRSMANEANSEEAITPQ  
501 QQQQQQ---MARSSQEEKKEKEKEADKEEKEQDAENEKEELSKEKTDGSDNDEKEAVASKGRKTANSQGRRKGRITRSMANEANHEETATPQ

601 SAELASMELESSSRWTEEMETAKKGLLEHGRNWSAIARMVSGKTSVQCKNFYFNKQRNLDLQHKLMKEKERNARRKKKAPAAASEEAFPPV  
597 SSELASMEMNESSRWTEEMETAKKGLLEHGRNWSAIARMVSGKTSVQCKNFYFNKQRNLDLQHKLMKEKERNARRKKKTPAAASEETAPFAA

701 EDEEMEASGVSGNEEMVEAEALHASGNEVPR-GECSGPATVNNSSDTEISPSHTEAAKDTGQNGPKPPATLGADGPPGPPTPPRRTSRAPIEPTA  
697 EDEEMEASGASANEELAEAEASQASGNEVPRVGECSGPAVNNSSDTEISVSPSRSEAMKDTG---PKPTGTEALPAATQPPVPPPEEPAVAPAEPSV

800 SEATGAPTPPPAPPSPSAPPVVPKEEKEETAAPP--VEEGEEQKPPAAE-LAVDTGKAEEP---VKSECTEEAEEGA-KGKDAEAAEATAEGALK  
794 PDASGPPSPPEPSSHLP-PRLLWTRMNNKPRLLQLPRQMPRSRSLRPRRSMWEKPEEPEASEEPPESVKSDHKEETEEEDKAKGTEAETVSEAPLK

893 AEKKEGSGRATTAKSSGAPQSDSSATCSADEVDEAEGDKNRLSPRPSLLTPTGDPANASPOKPLDLKQLKQRAAIPPIQVTKVHEPPREDAPT  
893 VEE-AGSKAAVTGSSSGATQSDSFATCSADEVDEPEGGDKRLLSPRPSLLTPAGDPRASTSPQKPLDLKQLKQRAAIPPIQVTKVHEPPREDTVP

993 KPAPPAPPPQNLQPEDAPQQPGSSPRGKSRSPAPPADKEA-----FAAEAKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPGPHL  
992 KPVPVPPPTQLQPEGDVSSQSGSPRGKSRSPVPAEKEAEKPAFFPAPPTGPKLPTTEPRWSSGLPFPPIPPREVIKTSPHAADPSAFSYTPGPHL

1095 PLGLHDTARVLP RPPTISNPPPLISSAKHPSVLERQIGAIQS-GMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPPSGVKQEQLSPRGQAGPPES  
1092 PLGLHDSARPVLP RPPTISNPPPLISSAKHGPVLERQLGAISQQGMSVQLRVPHSEHAKAPMGPLTMGLPLAVDPKKL-----

1184 LGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDAITYRGSITHGTADVLKYGTITRIIGEDSPSRDLRGREDSLPKGHVIEGKKGHVLSYEGG  
1169 -----GTALGSATSGSITKGLPSTRAADGPS--YRGSITHGTADVLKYGTISRIVGEDSPSRDLRAREDTPKGHVIEGKKGHVLSYEGG

1284 MSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRASSASIEGLMGRAIPPERHSPHLKEQHHRGSIQTGIPRSYVEAQEDYLREAKLLKREGT h-SMRT  
1254 MSVSQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRVTSASIEGLMGRAIP-EQHSPL-LKEQHHRGSIQTGIPRSYVEAQEDYLREAKLLKREGT m-SMRT

1384 PPPPPSRDLTEAYKT---QALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTGSKKHVDVRSIGSP h-SMRT  
1352 PPPPPSRDLTETKYPRPLDPLGPKLKPTHEGVVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDSGAPSTGKKHVDVRSIGSP m-SMRT

1481 GRTFPPVHPLDVMADARALERACYEESLKSRTGASSSGGSIARGAPVIVPELKGPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSKAS h-SMRT  
1452 GRFPFALHPLDIMADARALERACYEESLKSRTGSSGAGGSITRGAPVVVPELKGPRQSPLTYEDHGAPFTSHLPRGSPVTMREPTPRLQEGSLSSSKAS m-SMRT

1581 QDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLRGVSGVDLYRSHIPLAFDPTSIPRGIPLDAAA-YLPRHLAPNPTYPHLYPPYLIRGYPDAAAL h-SMRT  
1552 QDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLRGVGTVDLYRSHIPLAFDPTSIPRGIPLEAAAAAYLPRHLAPNPTYPHLYPPYLIRGYPDAAAL m-SMRT

1690 ENRQTIINDYITSQMHNTATAMARADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPPTGTPATAMDRLAYLPTAPQPFSSRHSSSPLSP h-SMRT  
1652 ENRQTIINDYITSQMHNTAASAMARADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPPTGTPATIDRLAYLPTAPQPFSSRHSSSPLSP m-SMRT

1780 GGPHTLTKPTTTSSSERERDRDRERDREREKSIILSTTTVEHAPIWRPGTEQSSGSSGSSGSSGSSRPAHSHAHQHSPISPRTQDALQORPSVLH h-SMRT  
1752 GGPHTLAKPTATSSSERERERERERD-----KSILSTTTVEHAPIWRPGTEQSSGAGGSS-----RPASHTQH--SPISPRTQDALQORPSVLH m-SMRT

1680 NTGMKGIIITAVEPSKPTVLR---STSTSSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPS h-SMRT  
1836 NTSKMGVTSVEPGTPTVLRWARSTSTSSPVRPAATFPPATHCPLGGTLEGVYPTLMEPVLLPKETS RVARPERARVDAGHAFLTKPPGR---EPASSPS m-SMRT

1977 KGSEPRPLVPPVSGHATIARTPAKNLAPHASPDPPAPPASADPHREKTQSKPFSIQELELRLSGYH-GSSYSPEGVEPVSPVSSPSLTHDKGLPKHLE h-SMRT  
1933 KSSEPRSLAPPSSSHTAIARTPAKNLAPHASPDPPAPT-SASDLHREKTQSKPFSIQELELRLSGYHSGAGYSPDGVEPISPVSFSLTHDKGLSKPLE m-SMRT

2076 ELDKSHLEGELRPKQPGPVKLGGAAHLPHLRPLPESQPSSSPLLQTPAGVKGHQVRVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLD h-SMRT  
2032 ELEKSHLEGELRHKQPGPMKLSAAEAHLPHLRPLPESQPSSSPLLQTPAGIKGHQVRVTLAQHISEVITQDYTRHHPQQLSGPLPAPLYSFPGASCPVLD m-SMRT

2176 LRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHRSASVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKL h-SMRT  
2132 LRRPPSDLYLPPPDHGTPARGSPHSEGGKRSPEPKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQCEPR-MGLESFGNTSQPPTFFSKL m-SMRT

2276 TESNSAMVSKKQEIINKLNTNHRNEPEYNISQPGTEIFNMPAITGTGLMITYRSQAVQEHASTNMGLEAIIIRKALMGKYDQWEEPPLSANAFNPLNASE h-SMRT  
2231 TESNSAMVSKKQEIINKLNTNHRNEPEYNISQPGTEIFNMPAITGAGLMTCRSQAVQEHASTNMGLEAIIIRKALMGKYDQWEEPPLGANAFNPLNASE m-SMRT

2376 SLPAA-MPITAADGRSDHTLTPGGGGKAKVSGRPSRRKAKSPAGLASGDRPPSVSSVHSEGDENRRTPLTNRVWEDRPSSAGSTFPFYNPLIMRLQAG h-SMRT  
2331 SLPAAAMPITADGRSDHALTPGGGGKAKVSGRPSRRKAKSPAGLASGDRPPSVSSVHSEGDENRRTPLTNRVWEDRPSSAGSTFPFYNPLIMRLQAG m-SMRT

2475 VMASPPPPGLPAGSGPLAGPHHAWDEEPPKLLCSQYETLSDSE h-SMRT  
2431 VMASPPPPGLAAGSGPLAGPHHAWDEEPPKLLCSQYETLSDSE m-SMRT

FIGURE 4

**FIGURE 5A**

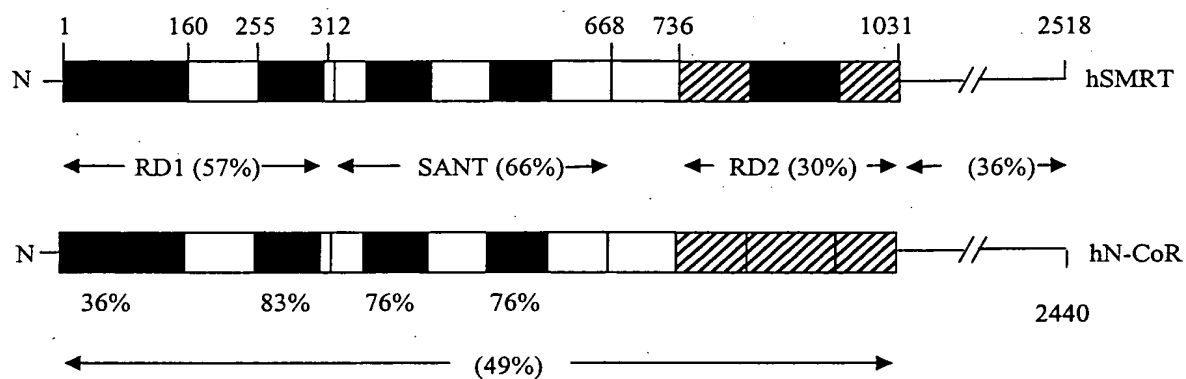


FIGURE 5B



FIGURE 6A

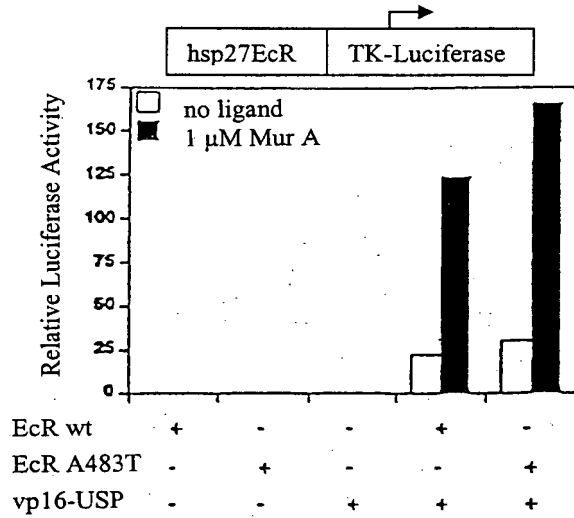


FIGURE 6B

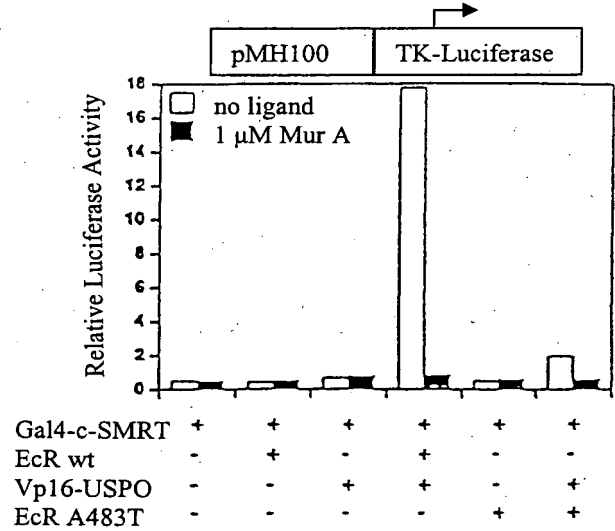
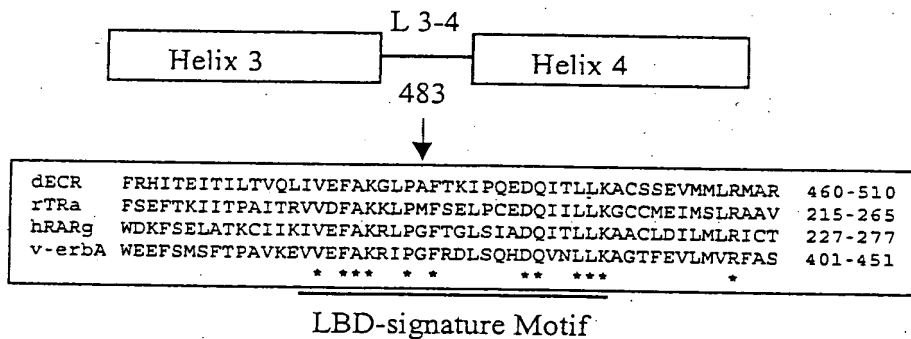


FIGURE 6C





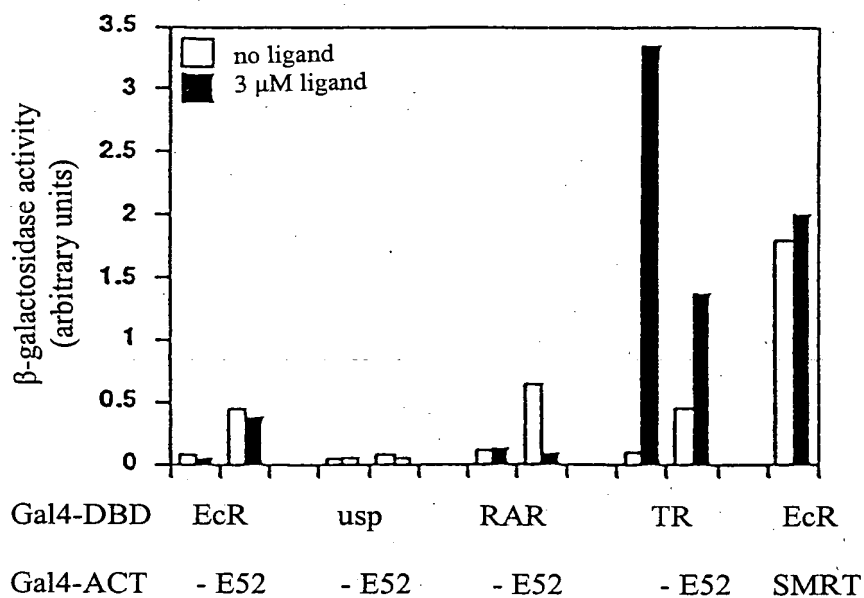


FIGURE 7

[illegible]



### SNOR motif

SMRTER:	573	KEELLMQIQKVDNEIKSAETTMTLKKKEKSLMEEAALAKEQRAAKELND
mN-CoR:	177	KEELIQSMDRVVDREIAKVEQQIILKLLKKKQQQLEEEA--AKPPEPEKPVSP
hSMRT:	169	KEELIQNMDRVVDREITMVEQQISKLKKKQQQLEEEA--AKPPEPEKPVSP
SMRTER:	623	NNNDQEPMVLSWRSQMLAEKTYAANRRKTAQAQHSMLQNAADESSPGSV
mN-CoR:	226	-----PFVEQKHRS--IVQIIYDENRKKAELEAHKIFEGGLGPKVE-----
hSMRT:	217	-----PPTESKHRS--LVQIIYDENRKKAEAAHRILEGGLGPOVE-----
SMRTER:	673	AGRPWLPLYNQHLVDVEALAMLIHQHOSQIRAPILLHIRKLLKAEKRWANNQ
mN-CoR:	263	-----LPLYNQPSDTRFYHENIKINQV-MRKKLILFKRRNHARKQREKQ
hSMRT:	254	-----LPLYNQPSDTRFYHENIKINQA-MRKKLILFKRRNHARKQWKQK
SMRTER:	723	LVEKYTKDQADWQRRICERMEASAKRKAREAKNREFFEKVFTELRKQREOK
mN-CoR:	307	ICORYDQLMFAWEKKVDRIENNPRRKAKESKTREYYEKQFPETRKQREQQ
hSMRT:	298	FCORYDQLMFALEKKVERIENNPRRKAKESKVREYYEKQFPETRKQRELO
SMRTER:	773	ERFN-RVGSR-----IKSEADLEEIMDGLQEQALEDKMRSYAVIPP
mN-CoR:	357	ERFQ-RVGQRGAGLSATIRSEHEISEIIDGLSEQENNEKQMRQLSVIPP
hSMRT:	348	ERMOSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPP
SMRTER:	814	LMHDARQRRCAVHNENGLIEDMVAVHQQRKALNM
mN-CoR:	406	MMFDARQRRVVKFINMNGLMEDPMKVYKDRQFMNV
hSMRT:	398	MLYDADQRIKFINMNGLMADPMKVYKDRQVMNM

### SANT domain

SMRTER	:848	WTAGEKETFKKYLQHPKNFGATAASLDR-KSPQDCVRYFYLSKKKTENY	100%
mN-CoR(1)	:440	WTDHEKEIFKDKFIQHPKNFGLIASYLER-KSVPCVLYFYLTKKKNENY	68/80%
hSMRT(1)	:432	WSEQEKETFREKFMQHPKNFGLIASFLER-KTVAECVLYFYLTKKKNENY	64/82%
C14B9.6	:615	WSPEERSLFSROADHVKIFHGLTEFFVD-KTASDLVLFYFMNKKTEDY	35/53%
Cf53H10	:218	WTPDEIYQFQDAIYQSEKDFDKVAVELPG-KSVMECVQFYTWKKDCPD	38/56%
xER1	:277	WTEEECRNFEQGLKAIGKDFHLITQANKVTRTSVGECVAFYMWKKSERV	36/56%
mN-CoR(2)	:627	WTEEEEMEVAKKGLVEHGRNWAATAK-MVGTKSEADCKNFYFNKRRHNL	34/53%
hSMRT(2)	:615	WTEEEEMETAKKGLLEHGRNWSATAK-MVGSHTVSQCKNFYFNKRRNL	38/57%
hKIAA0071	:106	WTVKDKVLFQAFSPFKIFPHRIQOMLPD-KSIASLVKFFYSWKKIRTK	37/50%
CMTA-I	:198	WTDQETITLFENCYQIFGKNFSQIRSEALCH-RSLOSIVQFYYESKKRVKY	39/51%
YCR592	:673	ETDHEHSLFLEGYLITHEKIFGKISHVMGGLRSPEDCVLHYRTKKTVNY	46/62%

α-helix

α-helix

### ITS motif

SMRTER:	2424	TRQIVMHDYITSQQMO
SMRT:	1681	NROTIINDYITSQQMH
N-CoR:	1615	TRQTIINDYITSQQMO

### GSI motif

SMRTER:	2274	VKSGSIIHGTPANS
	2236	GKHGSITQGTPLHM
SMRT:	1203	VPGGSITKGTIPSTR
	1224	TYRGSITHGTPADV
	1350	HIRGSITQGTIPRSY
	1446	LKEGSITQGTPLKY
	1517	SSGGSIIARGAPVIV
N-CoR:	921	TPPGSILISSPIKP
	1064	IMGGSISQGTPTGT
	1092	PSVGSISLGLPRQO
	1149	VQEGSITRGTPASK
	1171	SLRGSITQGTPLP
	1302	VLSGSIMOGTTPRAT
	1388	IIEGSISQGTPIKF
C14B9.6:	920	QTQGSLSGTPTFQA

### LSD motif

SMRTER:	3430	ESKPLLSKYDALSD-ED
SMRT:	2501	EPKPLLSQYETLSDS
N-CoR:	2436	EPAPLLSAQYETLSDSDD

FIGURE 9

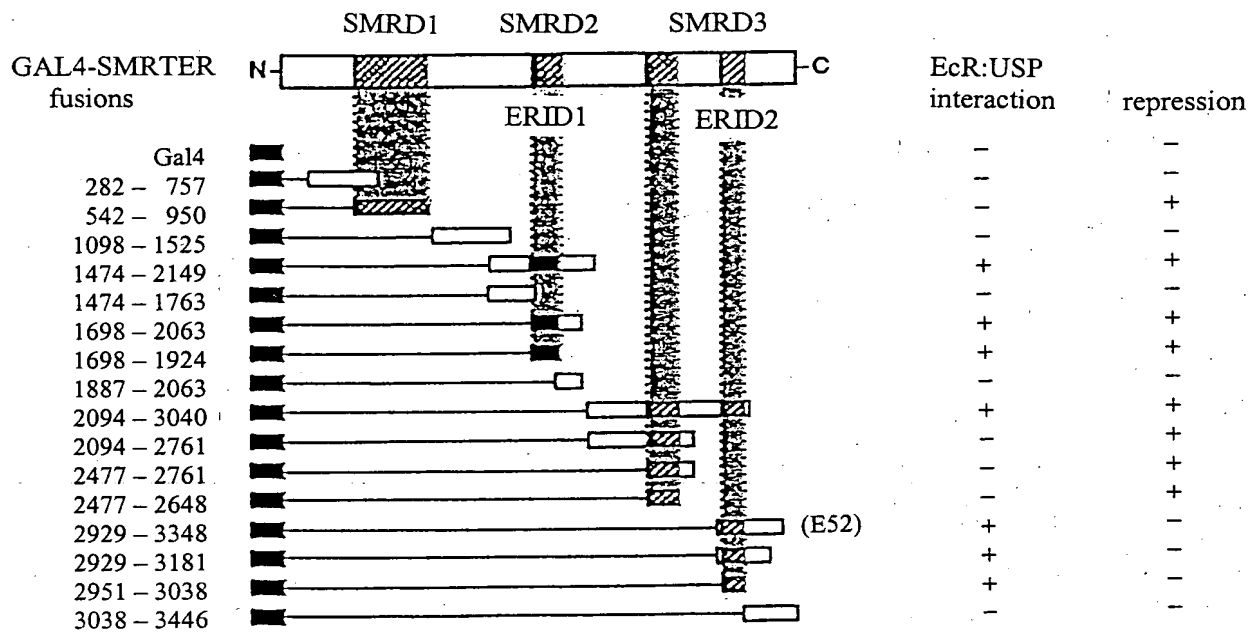


FIGURE 10



FIGURE 11A

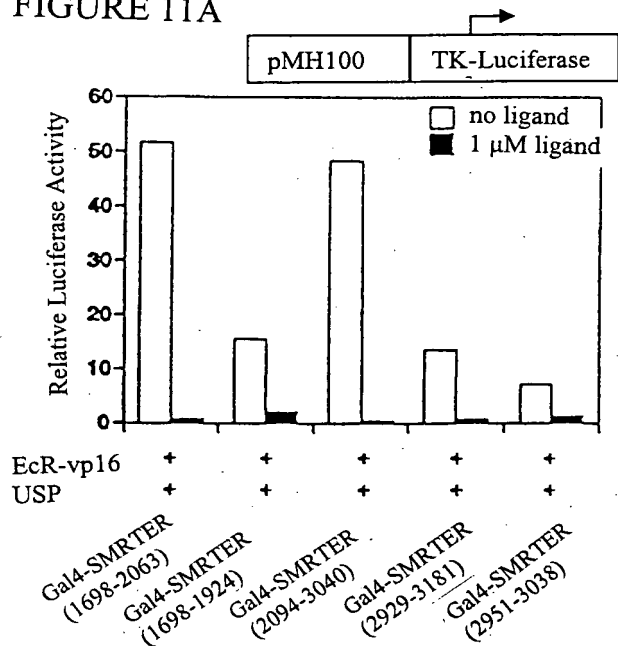


FIGURE 11B

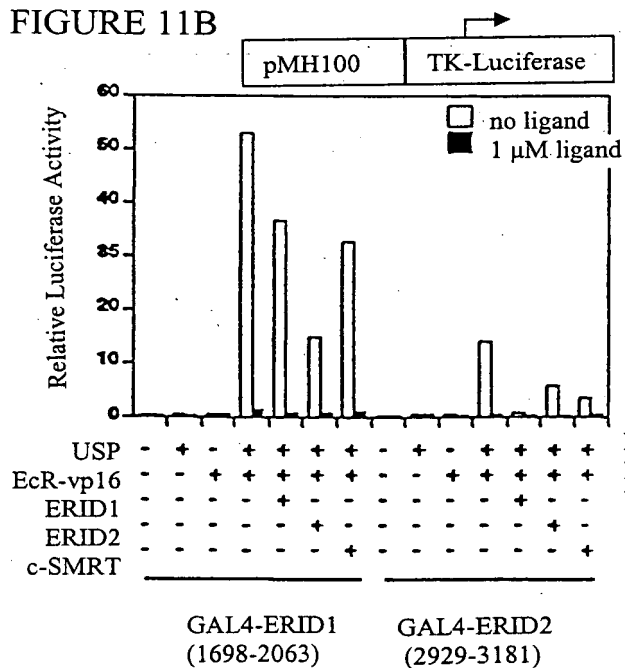


FIGURE 11C

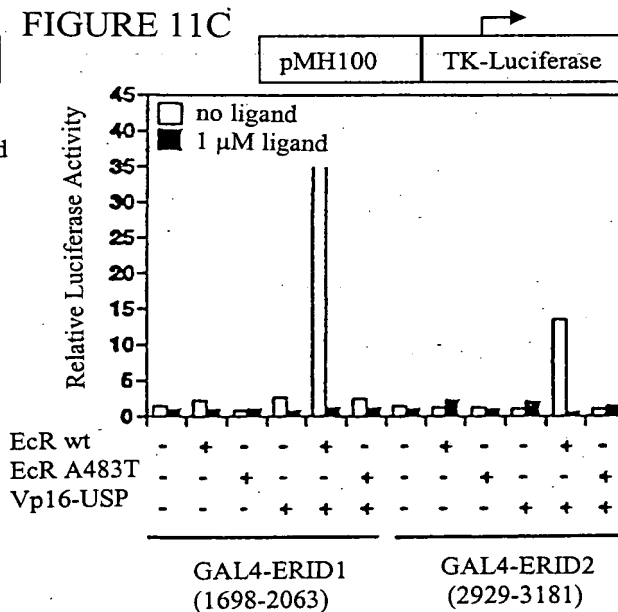


FIGURE 12A

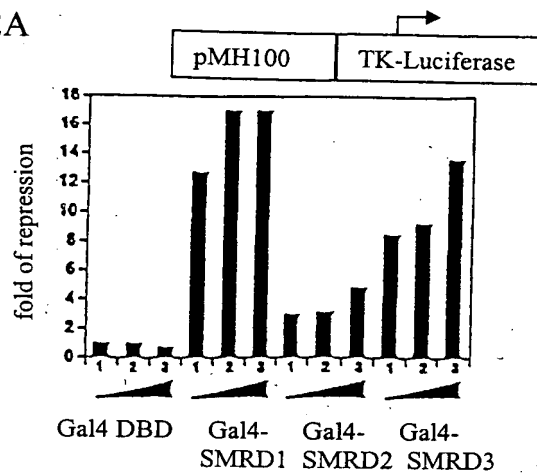


FIGURE 12B

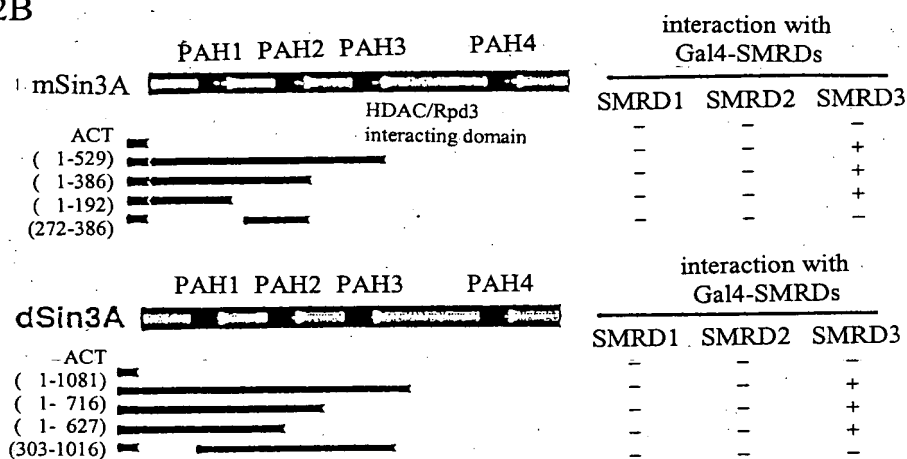


FIGURE 12C

